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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Mack, David H.
- (ii) TITLE OF INVENTION: COMPUTER-AIDED VISUALIZATION OF
EXPRESSION COMPARISON
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Joe Liebeschuetz of Townsend and Townsend and
Crew LLP
 - (B) STREET: Two Embarcadero Center, Eighth Floor
 - (C) CITY: San Francisco
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/020,743
 - (B) FILING DATE: 09-FEB-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Liebeschuetz, Joe
 - (B) REGISTRATION NUMBER: 37,505
 - (C) REFERENCE/DOCKET NUMBER: 018547034800US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650) 326-2400
 - (B) TELEFAX: (650) 326-2422

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2691 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAGACAGAC AGACAGCTGG CAAGAGGCAG CCTGGGGGCC ACAGCTGCTT CAGCAGACCT	60
CATGGCTGAG TGAGCCTCCC CTGGGCCCAG CACCCACCT CAGCATGGTC CAAGCCCATG	120
GGGGGCGCTC CAGAGCACAG CCGTTGACCT TGTCTTTGGG GGCAGCCATG ACCCAGCCTC	180
CGCCTGAAAA AACGCCAGCC AAGAAGCATG TGCGACTGCA GGAGAGGCGG GGCTCCAATG	240
TGGCTCTGAT GCTGGACGTT CGGTCCCTGG GGGCCGTAGA ACCCATCTGC TCTGTGAACA	300
CACCCCGGGA GGTCAACCTA CACTTTCTGC GCACTGCTGG ACACCCCTT ACCCGCTGGG	360
CCCTTCAGCG CCAGCCACCC AGCCCAAGC AACTGGAAGA AGAATTCTTG AAGATCCCTT	420
CAAACCTTGT CAGCCCCGAA GACCTGGACA TCCCTGGCCA CGCCTCCAAG GACCGATACA	480
AGACCATCTT GCCAAATCCC CAGAGCCGTG TCTGTCTAGG CCGGGCACAG AGCCAGGAGG	540
ACGGAGATTA CATCAATGCC AACTACATCC GAGGCTATGA CGGGAAGGAG AAGGTCTACA	600
TTGCCACCCA GGGCCCCATG CCCAACACTG TGTCGGACTT CTGGGAGATG GTGTGGCAAG	660
AGGAAGTGTC CCTCATTGTC ATGCTCACTC AGCTCCGAGA GGGCAAGGAG AAATGTGTCC	720
ACTACTGGCC CACAGAAGAG GAAACCTATG GACCCTTCCA GATCCGCATC CAGGACATGA	780
AAGAGTGCCC AGAATACACT GTGCGGCAGC TCACCATCCA GTACCAGGAA GAGCGCCGGT	840
CAGTAAAGCA CATCCTCTTT TCGGCCTGGC CAGACCATCA GACACCAGAA TCAGCTGGGC	900
CCCTGCTGCG CCTAGTGGCA GAGGTGGAGG AGAGCCCGGA GACAGCCGCC CACCCCGGGC	960
CTATCGTAGT CCACTGCAGT GCAGGGATTG GCCGGACGGG CTGCTTCATC GCCACGCGAA	1020
TTGGCTGTCA ACAGCTGAAA GCCCGAGGAG AAGTGGACAT TCTGGGTATT GTGTGCCAAC	1080
TGCGGCTAGA CAGAGGGGGG ATGATCCAGA CGGACGAGCA GTACCAGTTC CTGCACCACA	1140
CTTTGGCCCT GTATGCAGGC CAGCTGCCTG AGGAACCCAG CCCCTGACCC CTGCCACCCT	1200
CCGGTGGCCC AGGTGCCTAC CTCCCTCAAG CCTGGGAAGT CACAGGAAGC AGCAGCAGTA	1260
AGGACAAGGG GCCGGATTCC AGGTCTTCAA CACTGGCCAC TCCTCTGCTT CCTCTGTTGG	1320
CCCCAGATGG ACAGTAAGGG GAACCTCCAA TGTCTCTCTG AACTTAAAGA CAGGAGCTGG	1380
CATTTATGAC AGACAAAGAA AGAAGCCAG GTGTCTGCTT GTTCTCTGAG AACTCTTTG	1440
TGAGCTTCAG TTTCTGTTC TATAACATGA ACATAAGTGC TTAGCTGCCA TGAGGGAAAA	1500
GTAATGAGAG AAGTTTCTAG AAGCCACTCC AGCCACTCCT TCCTGGGGCT GACAAAAGGG	1560
TGATTCCAAG ATCATCCTTC ACCCGAGGTC CTGCCCAAGC ACAGGCCAGA TGCAAGAATG	1620
GGGAAAAGTC TGGTCCTGAT CTCCAAGTCT CAACATCCTA TCAGTGAATC TGCTCCCTGA	1680
CCACACATCG GAAGGGCTGG ATGACCCCAA TCAAAAGAAA GAACAAGGAC TCTGGTTACC	1740

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CTTGCCCTCC	ACCCATGTGT	CATAAGAGTA	GGCTACAGAG	GTGACCAGGC	CTGGCAGTTG	1800
AAATCTCTGG	AAGAGGGAAC	ATGTGGGGAC	TACTCAGAGG	CAAAGAGGAG	CTGCTCCTGC	1860
CTCCATGGTT	GCTGGCCACT	CCCACCAACT	ACTCTTAGGG	AGGCTAAGCA	GTCTCTGTTT	1920
TGCTTCCATG	GCTCAAATAA	TACCCTGGGT	ATGCAGGACC	CACTATACCT	TGCATTTGCT	1980
GGTACACCTA	GAGAGCTTGG	CTGTTTCCAA	AAACAATCAG	GGTCATAACC	ATCCATGCAG	2040
ACATGGAGGC	TCGGCTGAAC	CAGGACTCCT	CACTGTCTAC	CTGAGAGAAT	GAGCACCCCT	2100
CATCCATCTC	AGCATCAACA	CAATTTCCAG	GGGACCTCAG	GTCTACCTCA	GGACTGAACG	2160
CCACACCTCA	GGATTCCCTC	TCCTTGAATC	TGAGACTGGC	TGCCCATTCT	GAGATGGGGA	2220
TGAAGGTAAG	ATGCCGCATC	ACCAGGCACG	CCGCCCCTGA	CAGCTGCCTT	GATACCAGCT	2280
CTCTGTGGAA	ACCCCCGAGG	AGTTGGATCT	GGAGAACAGC	TGGGCCTCCT	CACTCAGGAC	2340
TTCTCTCCTG	AAGAACACGC	AGTGCTAAAA	CTGAGGATGA	TTTCCCTAAT	GCTTCTGCTT	2400
GGCCTTATGG	AGGAGCTGCT	CCTTCCTTAC	AGCCTTGGGG	ATGGACTTGC	CCACACCTCC	2460
ACCTCCCCTG	AGCCCTGTGA	GAGGCACGAC	TGTCTATGCC	AATGAGGCTC	GGTGGGGGGC	2520
TCTCAAGTGC	CTGATCCTGC	CCTGGGCTCA	GAGCCAGCCC	AGAGGGAAGC	AACTGCACAG	2580
CCCCACAGGC	CCTCCCTGGC	ACTGTCCCCC	CAACCCCATC	TCAGAGCTCA	GAGGGTACAA	2640
GCTCCAGAAC	AGTAACCAAG	TGGGAAAATA	AAGACTTCTT	GGATGACTGA	C	2691

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Gln	Ala	His	Gly	Gly	Arg	Ser	Arg	Ala	Gln	Pro	Leu	Thr	Leu
1				5					10					15	
Ser	Leu	Gly	Ala	Ala	Met	Thr	Gln	Pro	Pro	Pro	Glu	Lys	Thr	Pro	Ala
		20						25					30		
Lys	Lys	His	Val	Arg	Leu	Gln	Glu	Arg	Arg	Gly	Ser	Asn	Val	Ala	Leu
		35				40					45				
Met	Leu	Asp	Val	Arg	Ser	Leu	Gly	Ala	Val	Glu	Pro	Ile	Cys	Ser	Val
	50					55					60				

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Asn	Thr	Pro	Arg	Glu	Val	Thr	Leu	His	Phe	Leu	Arg	Thr	Ala	Gly	His	
65					70					75					80	
Pro	Leu	Thr	Arg	Trp	Ala	Leu	Gln	Arg	Gln	Pro	Pro	Ser	Pro	Lys	Gln	
				85					90					95		
Leu	Glu	Glu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Asn	Phe	Val	Ser	Pro	Glu	
				100				105					110			
Asp	Leu	Asp	Ile	Pro	Gly	His	Ala	Ser	Lys	Asp	Arg	Tyr	Lys	Thr	Ile	
		115					120					125				
Leu	Pro	Asn	Pro	Gln	Ser	Arg	Val	Cys	Leu	Gly	Arg	Ala	Gln	Ser	Gln	
	130					135					140					
Glu	Asp	Gly	Asp	Tyr	Ile	Asn	Ala	Asn	Tyr	Ile	Arg	Gly	Tyr	Asp	Gly	
145					150				155						160	
Lys	Glu	Lys	Val	Tyr	Ile	Ala	Thr	Gln	Gly	Pro	Met	Pro	Asn	Thr	Val	
				165					170						175	
Ser	Asp	Phe	Trp	Glu	Met	Val	Trp	Gln	Glu	Glu	Val	Ser	Leu	Ile	Val	
			180					185					190			
Met	Leu	Thr	Gln	Leu	Arg	Glu	Gly	Lys	Glu	Lys	Cys	Val	His	Tyr	Trp	
		195					200					205				
Pro	Thr	Glu	Glu	Glu	Thr	Tyr	Gly	Pro	Phe	Gln	Ile	Arg	Ile	Gln	Asp	
	210					215						220				
Met	Lys	Glu	Cys	Pro	Glu	Tyr	Thr	Val	Arg	Gln	Leu	Thr	Ile	Gln	Tyr	
225					230					235					240	
Gln	Glu	Glu	Arg	Arg	Ser	Val	Lys	His	Ile	Leu	Phe	Ser	Ala	Trp	Pro	
				245					250					255		
Asp	His	Gln	Thr	Pro	Glu	Ser	Ala	Gly	Pro	Leu	Leu	Arg	Leu	Val	Ala	
			260					265					270			
Glu	Val	Glu	Glu	Ser	Pro	Glu	Thr	Ala	Ala	His	Pro	Gly	Pro	Ile	Val	
		275					280					285				
Val	His	Cys	Ser	Ala	Gly	Ile	Gly	Arg	Thr	Gly	Cys	Phe	Ile	Ala	Thr	
	290					295					300					
Arg	Ile	Gly	Cys	Gln	Gln	Leu	Lys	Ala	Arg	Gly	Glu	Val	Asp	Ile	Leu	
305				310						315					320	
Gly	Ile	Val	Cys	Gln	Leu	Arg	Leu	Asp	Arg	Gly	Gly	Met	Ile	Gln	Thr	
				325					330					335		
Asp	Glu	Gln	Tyr	Gln	Phe	Leu	His	His	Thr	Leu	Ala	Leu	Tyr	Ala	Gly	
			340					345					350			
Gln	Leu	Pro	Glu	Glu	Pro	Ser	Pro									
		355					360									